## SEQUENCE LISTING

<110> Salon et al, John A.

<120> DNA Encoding A Human Melanin Concentrating Hormone Receptor (MCH1) And Uses Thereof

<130> 1795/57453-C/JPW

<140> NotYetKnown

<141> 2001-07-05

<150> 09/610,635

<151> 2000-07-05

<160> 28

<170> PatentIn Ver. 2.1

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<211> 1269

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<213> Homo sapiens

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<210> 2

<211> 422

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<213> Homo sapiens

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Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp 20 25 30

Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro 35 40 45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala 50 55 60

Thr Gly Thr Gly Trp Met Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala 85 90 95

Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met 100 105 110

Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser 115 120 125

Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn 130 135 140

Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu 145 150 155 160

Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly 165 170 175

Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp 180 185 190

Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile 195 200 205

Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg 210 215 220 Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser 225 230 235 240

Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe 245 250 255

Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr
260 265 270

Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu 275 280 285

Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met 290 295 300

Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr 305 310 315 320

Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val 325 330 335

Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser 340 345 350

Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu 355 360 365

Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys 370 375 380

Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln 385 390 395 400

Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg
405 410 415

Thr Glu Ser Lys Gly Thr 420

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gggcatcgtg ggaaactcca cggtcatctt tgctgtggtg aagaagtcca agctacactg 240
gtgcagcaac gtccccgaca tcttcatcat caacctctct gtggtggatc tgctcttcct 300
gctgggcatg cctttcatga tccaccagct catggggaac ggcgtctggc actttgggga 360
aaccatgtgc accctcatca cagccatgga cgccaacagt cagttcacta gcacctacat 420
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cagtatcacc cctgtgtggc tctacgccag gctcattccc ttcccagggg gtgctgtggg 600
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caacgeggee atcagettgg getatgetaa cagetgeetg aacceetttg tgtacatagt 960
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ctgacaattc cccagtcgcc tccaagtcag gccaccccat caaaccgtgg ggagagatac 1140
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<211> 353

<212> PRT

<213> Rattus norvegicus

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Ile Ser Asp Gly Gln Asp Asn Leu Thr Leu Pro Gly Ser Pro Pro Arg
20 25 30

Thr Gly Ser Val Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe Gly
35 40 45

Thr Ile Cys Leu Leu Gly Ile Val Gly Asn Ser Thr Val Ile Phe Ala
50 55 60

Val Val Lys Lys Ser Lys Leu His Trp Cys Ser Asn Val Pro Asp Ile
65 70 75 80

Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly Met 85 90 95

Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe Gly 100 105 110

- Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe 115 120 125
- Thr Ser Thr Tyr Ile Leu Thr Ala Met Thr Ile Asp Arg Tyr Leu Ala 130 135 140
- Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Met Ala 145 150 155 160
- Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr
  165 170 175
- Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val 180 185 190
- Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe 195 200 205
- Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile 210 215 220
- Thr Ala Ala Tyr Val Lys Ile Leu Gln Arg Met Thr Ser Ser Val Ala 225 230 235 240
- Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg 245 250 255
- Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr 260 265 270
- Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr 275 280 285
- Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser 290 295 300
- Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys 305 310 315 320
- Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg Thr 325 330 335
- Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg Thr Glu Ser Lys Gly 340 345 350

Thr

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	<212> DNA		
	<213> Artificial Sequence		
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	<220>		
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	<210> 6		
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	(213) Altitudat boquonee		
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<u>I</u>	<400> 6		
11.5 11	tagcggtcaa tggccatggc ggtcag	26	
T <u>i</u>			
<b>2</b>	<210> 7		
a	<211> 45		
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E	(223) Description of Artificial Sequence. Plane, plane		
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	ctcctgggca tgcccttcat gatccaccag ctcatgggca atggg	45	
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j	<223> Description of Artificial Sequence: primer/probe	
j	•	
<b>]</b>	<400> 10	
oline Vandi Umdi Umdi Umdi Umdi U	cgcggatcca ttatgtctgc actccgaagg aaatttg	37
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,		
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	cgcgaattet tatgtgaage gateagagtt cattttte	36
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Į	<223> Description of Artificial Sequence: primer/probe	
₩ <b>T</b>	<400> 14	
## ##	tcagctcggt tgtgggagca	20
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4	<213> Artificial Sequence	
though the state that the state that	(213) Altificial bequese	
4	<220>	
ii) ia	<223> Description of Artificial Sequence: primer/probe	
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	<210> 16	
	<211> 100	
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	MCH1	

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Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp 20 25 30

Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro 35 40 45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala 50 55 60

Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly 65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala 85 90 95

Gly Ser Pro Pro 100

<210> 17

<211> 100

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: mutated human MCH1

<400> 17

Met Ser Val Gly Ala Ala Lys Lys Gly Val Gly Arg Ala Val Gly Leu
1 5 10 15

Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp 20 25 30

Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
50 55 60

Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly 65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala

Gly Ser Pro Pro

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<213> Artificial Sequence
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<223> Description of Artificial Sequence: primer/probe
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                                                                   31
cgaggettee aggteegeec agecagtgee g
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<210> 21
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<212> DNA
<213> Artificial Sequence
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<223> Description	of Artificial	Sequence:	primer/probe	
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		•		
010. 00				
<210> 22 <211> 33				
<211> 33 <212> DNA				
<213> Artificial S	Sequence			
	-			
<220>				
<223> Description	of Artificial	Sequence:	primer/probe	
•			•.	
<400> 22				33
taatgtgtct aggtgg	grc agrgggage	catg		33
•				
<210> 23				
<211> 33				
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.400. 22				
<400> 23 catggetece actgace	rcca cotagação	a tta		33
catggettee actgate	,cou coungication			*
	·			
<210> 24				
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(223) Description	OI MICILICIAL	Doğumus.	<b>P</b>	
<400> 24	•	•		
tgacactaag cttcact	ggc tggatggac	tggaagc		37
,				
	•			
<210> 25				
<211> 24				
<212> DNA	lomionae	•		
<213> Artificial S	edneuce			
<220>				
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## <223> Description of Artificial Sequence: primer/probe

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24

<210> 26

<211> 422

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: mutated human MCH1

<400> 26

Met Ser Val Gly Ala Met Lys Lys Gly Val Gly Arg Ala Val Gly Leu

1 5 10 15

Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp 20 25 30

Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro 35 40 45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala 50 55 60

Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala 85 90 95

Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met 100 105 110

Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser 115 120 125

Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn 130 135 140

Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu 145 150 155 160

Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly 165 170 175

Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp 180 185 190

Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile 195 200 205

Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg 210 215 220

Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser 225 230 235 240

Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe 245 250 255

Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr 260 265 270

Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu 275 280 285

Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met 290 295 300

Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr 305 310 315 320

Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val 325 330 335

Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser 340 345 350

Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu 355 360 365

Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys 370 375 380

Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln 385 390 395 400

Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg 405 410 415

Thr Glu Ser Lys Gly Thr 420 <210> 27

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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: mutated human MCH1

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Met Ser Val Gly Ala Ala Lys Lys Gly Val Gly Arg Ala Val Gly Leu
1 5 10 15

Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp 20 25 30

Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro 35 40 45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala 50 55 60

Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly 65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala 85 90 95

Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met 100 105 110

Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser 115 120 125

Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn 130 135 140

Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu 145 150 155 160

Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly 165 170 175

Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp 180 185 190

- Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile 195 200 205
- Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg 210 215 220
- Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser 225 230 235 240
- Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe 245 250 255
- Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr 260 265 270
- Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu 275 280 285
- Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met 290 295 300
- Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr 305 310 315 320
- Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val 325 330 335
- Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser 340 345 350
- Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu 355 360 365
- Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys 370 375 380
- Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln 385 390 395 400
- Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg 405 410 415

Thr Glu Ser Lys Gly Thr 420

<210> 28 <211> 353 <212> PRT

<213> Artificial Sequence

<220>

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<400> 28

Met Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly Pro Asn Ala Ser Asn 1 5 10 15

Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala Gly Ser Pro Pro Arg
20 25 30

Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe Gly 35 40 45

Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser Thr Val Ile Phe Ala 50 55 60

Val Val Lys Lys Ser Lys Leu His Trp Cys Asn Asn Val Pro Asp Ile 65 70 75 80

Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly Met 85 90 95

Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe Gly
100 105 110

Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe 115 120 125

Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile Asp Arg Tyr Leu Ala 130 135 140

Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Val Ala 145 150 155 160

Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr 165 170 175

Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val 180 185 190

Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe 195 200 205

Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile



Thr	Ala	Ala	Tyr	Val	Arg	Ile	Leu	Gln	Arg	Met	Thr	Ser	Ser	Val	Ala
225					230					235					240

Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg 245 250 255

Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr 260 265 270

Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr 275 280 285

Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser 290 295 300

Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys 305 310 315 320

Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg Ala 325 330 335

Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg Thr Glu Ser Lys Gly 340 345 350

Thr